REMARKS

I.   Status of the Claims

Applicants respectfully request reconsideration of the present application in view of the foregoing amendments and in view of the reasons that follow.

In the specification, paragraphs have been amended on pages 41, 42, 70, 71, 72, 74, 76, 80, 88, 90, 91, 96.

Claims 1 – 8, 18 – 20 and 26 – 27 are requested to be cancelled. The cancellation of claims does not constitute acquiescence in the propriety of any rejection set forth by the Examiner. Applicants reserve the right to pursue the subject matter of the canceled claims in subsequent divisional applications.

Claims 11, 14 and 16 are currently being amended. Support for the amendments to claims 11, 14 and 16 is found in Figure 3 and SEQ ID NO: 36.

This amendment adds, changes and/or deletes claims in this application. A detailed listing of all claims that are, or were, in the application, irrespective of whether the claim(s) remain under examination in the application, is presented, with an appropriate defined status identifier.

After amending the claims as set forth above, claims 9 – 17 and 21 – 25 are now pending in this application.

II.   Response to Issues Raised by Examiner in June 30, 2004 Interview Summary

The Examiner acknowledges that to correctly view the sequence depicted in Figures 3a-3d, the pages should be placed side by side, as indicated by the illustration on page 3/15 of the Figures. Further to the Examiner's request, Applicants have amended the brief

description of Figure 3 to recite "[f]igure 3a should be viewed adjacent to Figure 3b and Figure 3c should be viewed adjacent to Figure 3d."

The Examiner also notes that residue 40 is a tryptophan in SEQ ID NO: 36 and a histidine in Figure 3a. As shown in Figure 3a (see Exhibit 1), the codon encoding amino acid residue 40 is TGG, which codes for tryptophan. However, due to a clerical error, histidine is listed as amino acid residue 40 in Figure 3a. Amino acid residue 40 in SEQ ID NO: 36 is correctly listed as tryptophan. Applicants will file corrected drawings shortly. No new matter has been added.

III.   Response to Issues Raised By Examiner In July 2, 2004 Communication

The Examiner states that "the claim(s) are directed to the amino acid sequences listed in Figure 3 which do not correspond to any of the sequences in the sequence listing nor do they have their own sequence identifier. In addition, the specific sequence that corresponds to Figure 3 needs to be recited in the claim(s) with the sequence identifier (i.e. SEQ ID NO), see claim 11." As discussed in detail above, Applicants note that SEQ ID NO: 36 corresponds to Figure 3. Applicants have amended the claims by replacing the term "Figure 3" with "SEQ ID NO: 36."

IV.   Issues Related to Figure 2 and SEQ ID NOS 33 and 34

Attached as Exhibit 2 is a copy of Figures 2a-f showing errors that have been corrected in the attached Sequence Listing (SEQ ID NO: 34). The errors relate to incorrect amino acids encoded by the recited codon. For example, the codon encoding amino acid residue 49 in Figure 2a is TTC, which codes for phenylalanine. However, due to a typographical error, tyrosine is listed as amino acid residue 49 in Figure 2a. Applicants will file corrected drawings shortly. No new matter has been added.

CONCLUSION

Applicants believe that the present application is now in condition for allowance. Favorable reconsideration of the application as amended is respectfully requested.

The Examiner is invited to contact the undersigned by telephone if it is felt that a telephone interview would advance the prosecution of the present application.

The Commissioner is hereby authorized to charge any additional fees which may be required regarding this application under 37 C.F.R. §§ 1.16-1.17, or credit any overpayment, to Deposit Account No. 19-0741. Should no proper payment be enclosed herewith, as by a check being in the wrong amount, unsigned, post-dated, otherwise improper or informal or even entirely missing, the Commissioner is authorized to charge the unpaid amount to Deposit Account No. 19-0741. If any extensions of time are needed for timely acceptance of papers submitted herewith, Applicants hereby petition for such extension under 37 C.F.R. §1.136 and authorizes payment of any such extensions fees to Deposit Account No. 19-0741.

Respectfully submitted,

Date 2 August 2004   By _____

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-14-

(35)

(36)

```
   1   GAATTCGGCACGAGCGGGCTGGACCTTGCTCGCCCGCGGCGCCATGAGCCGCAGCCTGGACTCGG
   1                                                M  S  R  S  L  D  S

 121   CGCCGGCGAGTTCAGCGACATCCAGGCCTGCTCGGCCGCCTGGAAGGCTGACGGCGTGTGCTCCA
  26     A  G  E  F  S  D  I  Q  A  C  S  A  A  H  K  A  D  G  V  C  S
                                                    W

 241   GCCTTATGATCAGACGCGAGTAATCCTCTCCCTGCTCCAGGAAGAGGGACACAGCGACTACATTA
  66     P  Y  D  Q  T  R  V  I  L  S  L  L  Q  E  E  G  H  S  D  Y  I

 361   ACCCTTGCCTCACACCCTGCTAGACTTCTGGAGACTGGTCTGGGAGTTTGGGGTCAAGGTGATCC
 106     P  L  P  H  T  L  L  D  F  W  R  L  V  W  E  F  G  V  K  V  I

 481   CCAGGAGCAGGAGCCACTGCAGACTGGGCTTTTCTGCATCACTCTGATAAAGGAGAAGTGGCTGA
 146     Q  E  Q  E  P  L  Q  T  G  L  F  C  I  T  L  I  K  E  K  W  L

 601   TGTGTACCAGCTACAGTATATGTCCTGGCCAGACCGTGGGGTCCCCAGCAGTCCTGACCACATGC
 186     V  Y  Q  L  Q  Y  M  S  W  P  D  R  G  V  P  S  S  P  D  H  M

 721   TGTCCACTGCAGTGCGGGTTGTGGGCGAACAGGCGTCCTGTGCACCGTGGATTATGTGAGGCAGC
 226     V  H  C  S  A  G  C  G  R  T  G  V  L  C  T  V  D  Y  V  R  Q

 841   GATGAGGAAGCAGCGGCCTGCGGCCGTGCAGACAGAGGAGCAGTACAGGTTCCTGTACCACACGG
 266     M  R  K  Q  R  P  A  A  V  Q  T  E  E  Q  Y  R  F  L  Y  H  T

 961   CAAAGAGAATTGTGCCCCACTCTACGACGATGCCCTCTTCCTCCGGACTCCCCAGGCACTTCTCG
 306     K  E  N  C  A  P  L  Y  D  D  A  L  F  L  R  T  P  Q  A  L  L

1081   GGGCCACGCCATGGCTGACACCTACGCGGAGGAGCAGAAGCGCGGGGCTCCAGCGGGCGCCGGGA
 346     G  H  A  M  A  D  T  Y  A  E  E  Q  K  R  G  A  P  A  G  A  G

1201   CTACAGCAAGGTGACGCCGCGCGCCCAGCGACCCGGGGCGCACGCGGAGGACGCGAGGGGGACGC
 386     Y  S  K  V  T  P  R  A  Q  R  P  G  A  H  A  E  D  A  R  G  T

1321   CGTGGCGGGTGGAGCTCAGACCGGTGGGCTAGGTTTCAACCTGCGCATTGGGAGGCCGAAGGGTC
 426     V  A  G  G  A  Q  T  G  G  L  G  F  N  L  R  I  G  R  P  K  G

1441   TGTTGCCTCTTGTGAGCTCGGACTGCTGATGCCCCGGTGCTGCTGAGCGCCGTGCCGAGAATGGA
1561   TGCCCAATGACTGTAGCATTCAAGGCTTGAGGCTGGAGGAGGTAGCTAGGGTATAGTGGCTGGTG
1681   TTATGAAGGGGAGAAAGGGACAGATGAGCTTCCGGAGACTGCTCTCCTCACCACACAGCACTAGTC
1801   GTGGATGGACACTTCGCCATCCAGGCAGAACTAAGCCAGGCATAACCACAGCCAAGCAGATTAAC
1921   AACCTGGACAGACAGCCAAAGCTTCAGAGATACAGTCCACAGGTGGACAAAGGATCCCCCAGCCA
2041   AAACACAGCCCCCAAAAGACAGACATCTCTGCTAGCTGGACAGCCAGGTGGACCCCCTAAGTTAG
2161   TCAGACCCCACTCCCTCAGGTGGGCTGGCTGGCTGACAGACCTTCTGGCCAGACAGACTCCTAAC
```

Fig. 3a

```
      AATTCCGGGCGCCAGTCCCGCTCCGCGCCGCGCCGCTCCGCTCCGGCTCGGGCTCCGGCT
      CGACCTCCAACCATGGCCCGTGCCCAGGCGCTCGTGCTGGCACTCACCTTCCAGCTCTGC
  1                        M  A  R  A  Q  A  L  V  L  A  L  T  F  Q  L  C

      GTGCCCTGCGAGTACAGCCAGGCCCAGTACGATGACTTCCAGTGGGAGCAAGTGCGAATC
  37  V  P  C  E  Y  S  Q  A  Q  Y  D  D  Y  Q  W  E  Q  V  R  I
                                            F

      TCCCAGCATGCCCCAGGCCAGCGAGCCCATGTCATCTTCCAGAGCCTGAGCGAGAATGAT
  77  S  Q  H  A  P  Q  Q  R  A  H  V  I  F  Q  S  L  S  E  N  D
         Q            G

      CGCGTCTACGTGCGCGTTAATGGGGGCCCCTGGCGAGTGCTGTGTGGAATATGACTGGA
 117  G  V  Y  V  R  V  N  G  G  V  L  A  S  A  V  W  N  M  T  G
      R                       P

      TATCAGGTGCTGTTTGAGGCCCTCATCTCCCCAGACCGCAGGGGCTACATGGGCCTAGAT
 157  Y  Q  V  L  F  E  A  L  I  S  P  D  R  R  G  Y  M  G  L  D

      GTGGAGGTCAACGCGGGCCAGAACGCGTCGTTCCAGTGCATGGCCGCGGGAGAGCCCATG
 197  V  E  V  N  A  G  Q  N  A  S  F  Q  C  M  A  A  G  E  P  N
                                                               M

      ACATCAGCCACCGGCTTCCTGGCCACTTTCCCGCTGGCTGCCGTGAGCCGCGCCGAGCAG
 237  T  S  A  T  G  F  L  A  T  F  P  L  A  A  V  S  R  A  E  Q

      ATCGTCAAGGAGCCCCCAACTCCCATCGCGCCCCCACAGCTGCTGCGTGCTGGCCCCACC
 277  I  V  K  E  P  P  T  P  I  A  P  P  Q  L  L  R  A  G  P  T

      GAGATTGAGTACCGCATGGCGCGCGGGCCCTGGGCTGAGGTGCACGCCGTCAGCCTGCAG
 317  E  I  E  Y  R  M  A  R  G  P  W  A  E  V  K  A  V  S  L  Q
                                                H

      CGTCCCGGAGACGGCGGCACTGGCCGCTGGGCCACCCCTCATCAGCCGCACCAAATGCGC
 357  R  P  G  D  G  G  T  G  R  W  A  T  P  H  Q  P  H  Q  M  R

      CTGCAGTGGGAACCACTGGGCTACAACGTGACGCGTTGCCACACCTATACTGTGTCGCTG
 397  L  Q  W  E  P  L  G  Y  N  V  T  R  C  H  T  Y  T  V  S  L

      GAGCAAGGTGTCAGCCGCTACACCATCAAGAACCTGCTGCCCTATCGGAACGTTCACGTG
 437  E  Q  G  V  S  R  Y  T  I  K  N  L  L  P  Y  R  N  V  H  V

      GATGAGGATGTGCCCAGTGGGATTGCAGCCGAGTCCCTGACCTTCACTCCACTGGAGGAC
 477  D  E  D  V  P  S  G  I  A  A  E  S  L  T  P  T  P  L  E  D
```

Fig. 2a

```
CGCCTCGGGCTGGGCTCGGGCTCCGGGGGCGGCGTCCCCGCGCCGGGCCCCGGGACGCGC   120
GCGCCGGAGACCGAGACTCCGGCAGCTGGCTGCACCTTCGAGGAGGCAAGTGACCCAGCA   240
 A  P  E  T  E  T  P  A  A  G  C  T  F  S  E  A  S  D  P  A
                                        E

CACCCTGGCACCCGGGCACCTGCGGACCTGCCCCACGGCTCCTACTTGATGGTCAACACT   361
 H  F  G  T  R  A  P  A  D  L  P  H  G  S  Y  L  M  V  N  T
    P

ACCCACTGTGTGCAGTTCAGCTACTTCCTGTACAGCCGGGACGGCACAGGCGGCACCCTG   481
 T  H  C  V  Q  F  S  Y  F  L  Y  S  R  D  G  T  G  G  T  L

TCCCACGGCCGTCAGTGGCACCAGGCTGAGCTGGCTGTCAGCACTTTCTGGCCCAATGAA   601
 S  H  G  R  Q  W  H  Q  A  E  L  A  V  S  T  F  W  P  N  E

GACATCCTGCTTCTCAGCTACCCCTGCGCAAAGGCCCCACACTTCTCCCGCCTGGGCGAC   721
 D  I  L  L  L  S  Y  P  C  A  K  A  P  H  F  S  R  L  G  D

CGCCAACGCTTCCTCTTGCAACGGCAGAGCGGGGCCCTGGTGCCGGCCGGGGCGTTCGGC   841
 R  Q  R  F  L  L  Q  R  Q  S  Q  A  L  V  P  A  Q  A  F  G
                                G                  G

GACCTGTACCGCTGTGTGTCCCAGGCCCCGCGCGGCGGCGTCTCTAACTTCCCGGAGCTC   961
 D  L  Y  R  C  V  S  Q  A  P  R  G  G  V  S  N  F  A  E  L
                                                    P

TACCTCATCATCCAGCTCAACACCAACTCCATCATTGGCGACGGGCCGATCGTGCGCAAG   1081
 Y  L  I  I  Q  L  N  T  N  S  I  I  G  D  G  P  I  V  R  X
                                                         K

ACCTACAAGCTGTGGCACCTCGACCCCGACACAGACTATGAGATCAGCGTGCTGCTCACG   1201
 T  Y  K  L  W  H  L  D  P  D  T  E  Y  E  I  S  V  L  L  T
                                  D

AGAGCCCATGAGGGCCCCAAAGGCCTGGCTTTTGCTGAGATCCAGGCCCGTCAGCTGACC   1321
 R  A  H  E  G  P  K  G  L  A  F  A  E  I  Q  A  R  Q  L  T

TGCTATCACTACACCCTGGGCAGCAGCCACAACCAGACCATCCGAGAGTGTGTGAAGACA   1441
 C  Y  H  Y  T  L  G  S  S  H  N  Q  T  I  R  E  C  V  K  T

AGGCTTGTCCTCACTAACCCTGAGGGGCGCAAAGAGGGCAAGGAGGTCACTTTCCAGACG   1561
 R  L  V  L  T  N  P  E  G  R  X  E  G  K  E  V  T  F  Q  T
                              K

ATGATCTTCCTCAAGTGGGAGGAGCCCCAGGAGCCCAATGGTCTCATCACCCAGTATGAG   1681
 H  I  F  L  K  W  E  E  P  Q  E  P  N  G  L  I  T  Q  Y  E
 M
```

Fig. 2b

```
      ATCAGCTACCAGAGCATCGAGTCATCAGACCCGGCAGTGAACGTGCCAGGCCCACGACGT
517   I  S  Y  Q  S  I  E  S  S  D  P  A  V  N  V  P  G  P  R  R

      ACCTACCTGTTCTCCGTGCGGGCCCGCACAGGCAAAGGCTTCGGCCAGGCGGCACTCACT
557   T  Y  L  F  S  V  R  A  R  T  G  K  G  F  G  Q  A  A  L  T

      GGCGAGTCTGAGAACACCATCACCGTGCTGCTGAGGCCGGCACAGGGCCGCGGTGCGCCC
597   G  E  S  E  N  T  I  T  V  L  L  R  P  A  Q  G  R  G  A  P

      TGGACAGGACTGCTTCCCAGTGCCATTGACCTTCGAGGCGGCGCTGGCCCCAGGCTGGTG
637   W  T  Q  L  L  P  S  A  I  D  L  R  G  G  A  G  P  R  L  V
             G

      GGTGACAACCAGACCTACCGAGGCTTCTGGAACCCACCACTTGAGCCTAGGAAGGCCTAT
677   G  D  N  Q  T  Y  R  G  F  W  N  P  P  L  E  P  R  K  A  Y

      ATTGCCAGGAAAGCTGCCTGCAAGGAAAGCAAGCGGCCCCTGGAGGTGTCCCAGAGATCG
717   I  A  R  K  A  A  C  K  E  S  K  R  P  L  E  V  S  Q  R  S

      CTGGGTGCCATCATTGTCATCATCCGCAAAGGGAAGCCGGTGAACATGACCAAGGCCACC
757   L  G  A  I  I  V  I  I  R  K  G  K  P  V  N  M  T  K  A  T

      CAGAGCACCCTGCAGGAGGACGAGCGGCTGGGCCTGTCCTTCATGGACACCCATGGCTAC
797   Q  S  T  L  Q  E  D  E  R  L  G  L  S  F  M  D  T  H  G  Y

      TCCCCGAGGCGTCCCTGTGGCCGGAAGGGCTCCCCATACCACACGGGGCAGCTGCACCCT
837   S  P  R  R  P  C  G  R  K  G  S  P  Y  H  T  G  Q  L  H  P

      GGCTTCAAGCAGGAGTATGAGAGCTTCTTTGAAGGCTGGGACGCCACAAAGAAGAAAGAC
877   G  F  K  Q  E  Y  E  S  F  F  E  G  W  D  A  T  K  K  K  D

      CACCCGATGCTGGGAGACCCCAATGCCGACTACATTAATGCCAACTACATAGATGGTTAC
917   H  P  M  L  G  D  P  N  A  D  Y  I  M  A  N  Y  I  D  G  Y
                                       N

      TGGCGTATGGTGTGGCAGGAGCACTGTTCCAGCATCGTCATGATCACCAAGCTGGTCGAG
957   W  R  M  V  W  Q  E  H  C  S  S  I  V  M  I  T  K  L  V  E

      AAGATTATGCTGGTGAAGACAGAGACCCTGGCTGAGTATGTCGTGCGCACTTTTGCCCTG
997   K  I  M  L  V  K  T  E  T  L  A  E  Y  V  V  R  T  F  A  L
```

Fig. 2c

ACCATCTCCAAGCTCCGCAATGAGACCTACCATGTCTTCTCCAACCTGCACCCAGGCACC 1801
 T I S K L R N E T Y H V F S N L H P G T

GAGATAACCACTAACATCTCTGCTCCCAGCTTTGATTATGCCGACATGCCGTCACCCCTG 1921
 E I T T N I S A P S F D Y A D M P S P L

ATCAGTGTGTACCAGGTGATTGTGGAGGAGGAGCGGGCGCGAGGCTGCGGCGGGACGAGG 2041
 I S V Y Q V I V E E E R A R G C G G T R

CACTACTTCGGGGCCGAACTGGCGGCCAGCAGTCTACCTGAGGCCATGCCCTTTACCGTG 2161
 H Y F G A E L A A S S L P E A M P F T V

CTCATCTACTTCCAGGCAGCAAGCCACCTGAAGGGGGAGACCCGGCTGAATTGCATCCGC 2281
 L I Y F Q A A S H L K G E T R L N C I R

GAGGAGATGGGGCTTATCCTGGGCATCTGTGCAGGGGGGCTTGCTGTCCTCATCCTTCTC 2401
 E E M G L I L G I C A G G L A V L I L L

GTCAACTACCGCCAGGAGAAGACACACATGATCAGCGCCGTGGACCGCAGCTTCACAGAC 2521
 V N Y R Q E K T H M M S A V D R S F T D
                                       I

AGCACCCGGGGAGACCAGCGCAGCGGTGGGGTCACTGAGGCCAGCAGCCTCCTGGGGGGC 2541
 S T R G D Q R S G G V T E A S S L G G

GCGGTGCGTGTCGCAGACCTTCTGCAGCACATCAACCAGATGAAGACGGCCGAGGGTTAC 2761
 A V R V A D L L Q H I N Q M K T A E G Y

AAGGTCAAGGGCAGCCGGCAGGAGCCAATGCCTGCCTATGATCGGCACGAGTGAAACTG 2881
 K V K G S R Q E P M P A Y D R M R V K L
                                              H   V

CACAGGTCAAAGCCACTTCATAGCCACTCAAGGGCCGAAGCCTGAGATGGTCTATGACTTC 3001
 H R S N H F I A T Q D P K P E M V Y D F
                            G

GTGGGCAGGGTGAAATGCTCACGGTACTGGCCGGAGGACTCAGACACCTACGGGGACATC 3121
 V G R V K C S R Y W P E D S D T Y G D I

GAGCGGAGAGGCTACTCTGCCCGGCACGAGGTCCGCCAGTCCCACTTCACAGCGTGGCCA 3241
 E R R G Y S A R H E V R Q S H F T A W P

Fig. 2d

```
      GAGCATGGCGTCCCCTACCATGCCACGGGGCTGCTGGCTTTCATCCGGCGGGTGAAGGCC
1037  E  H  G  V  P  Y  H  A  T  G  L  L  A  F  I  R  R  V  K  A

      CGTTGCTATATCGTCCTGGATGTGATGCTGGACATGGCAGAGTGTGAGGGCGTCGTGGAC
1077  G  C  Y  I  V  L  D  V  M  L  D  M  A  E  C  E  G  V  V  D
      H

      CAGTACATCTTCATTCATGATGCAATCCTGGAGGCCTGCCTGTGTGGGGAGACCACCATC
1117  Q  Y  I  P  I  H  D  A  I  L  E  A  C  L  C  G  E  T  T  I

      TCCTCCCAGCTGCGGGAAGAGTTCCAGACGCTGAACTCGGTCACCCCGCCGCTGGACGTG
1157  S  S  Q  L  R  E  E  F  Q  T  L  N  S  V  T  P  P  L  D  V

      CTGCCGCCCGACCGCTGCCTGCCCTTCCTCATCTCCACTGATGGGGACTCCAACAACTAC
1197  L  P  P  D  R  C  L  P  F  L  I  S  T  D  G  D  S  N  N  Y

      CCGCTGCAGAGCACCACGCCCGACTTCTGGCGGCTGGTCTACGATTACGGGTGCACCTCC
1237  P  L  Q  S  T  T  P  D  F  W  R  L  V  Y  D  Y  G  C  T  S

      CCAGAGCCAGGCCGGCAGCAATATGGCCTCATGGAGGTGGAGTTTATGTCGGGCACAGCT
1277  P  E  P  G  R  Q  Q  Y  G  L  M  E  V  E  F  M  S  G  T  A

      GACCTGCTGGTGCGGCACTTCCAGTTCCTGCGCTGGTCTGCATACCGGGACACACCTGAC
1317  D  L  L  V  R  H  F  Q  F  L  R  W  S  A  Y  R  D  T  P  D

      GATGGGCGCACCATCGTGCACTGCCTAAACGGGGGAGGACGCAGCGGCACCTTCTGCGCC
1357  D  G  R  T  I  V  H  C  L  N  G  G  G  R  S  G  T  F  C  A

      CAAACCCTCCGGAACTACAAACCCAACATGGTGGAGACCATGGATCAGTACCACTTTTGC
1397  Q  T  L  R  N  Y  K  P  N  M  V  E  T  M  D  Q  Y  H  F  C
```

```
GGGCACCCACTGCACACTCAGGGCCAGACCCACCATCCTGGACTGGCGAGGAAGATCAGT
TCTTGCTCCCCCTTCCACTGTGGGCAGGGCCTTTCGCTTGTCCCATGGGCGGGTGGTGGG
GTGCTGAGAGGCCTGGTGCTGCCTGGCAGAGTGACAAAGGCTCAGGACGGCTGGCTCTGG
GCAGAGAGCATCCCAGGCCAAGGTTCCCACTCAGCCTGCCCCCTCTGCATGTGGGTAGAG
AGCAGGTCTCAATTCTGATAGCCAGTGGGGCACACTGACTGTCCTCCCCAGGGGAACTGC
CACTTGCTTCCCTGATATGTGCTCTGACTTCCCTGAACCAGGATCTGCCTATTACTGCTG
CCTCTTCCTTTAATCTTCAGGCCTCACTGGCCTGTCCTGCTCAGCTTGGGCCAGTGACAA
CCGTTGTGGGGAGGGGCAGTGTTAGAGCAGGGCTGGTCATACCCTCTGGAGTTCAGAGCA
TCTCTTTAAAAATGGGGCAGGCCACACCCCCATTCCGTGCCTCAATTTCCCCATCTGTAAA
TGTAAAGCGCTTTGTAAATAAACGTGCTCTCTGAATGCCAAAAAAAAAAAAAAACAAAAAAA
```

Fig. 2e

```
TCCACCCCACCTGATGCCGGGCCCATTGTCATCCACTGCAGCGCGGGCACCGGCCGCACA  3361
 S  T  P  P  D  A  G  P  I  V  I  H  C  S  A  G  T  G  R  T

ATTTACAACTGTGTGAAGACTCTCTGCTCCCGGCGTGTCAACATGATCCAGACTGAGGAG  3481
 I  Y  N  C  V  K  T  L  C  S  R  R  V  N  M  I  Q  T  E  E

CCTGTCAGTGAGTTCAAGGCCACCTACAAGGAGATGATCCGCATTGATCCTCAGAGTAAT  3601
 P  V  S  E  F  K  A  T  Y  K  E  M  I  R  I  D  P  Q  S  N

GAGGAGTGCAGCATCGCCCTGTTGCCCCGGAACCGCGACAAGAACCGCAGCATGGACGTC  3721
 E  E  C  S  I  A  L  L  P  R  N  R  D  K  N  R  S  H M D  V

ATTAATGCAGCCCTGACTGACAGCTACACACGGAGGTCGGCCTTCATGGTGACCCTGCAC  3841
 I  N  A  A  L  T  D  S  Y  T  R  R  S  A  F  M  V  T  L  H

ATCGTCATGCTCAACCAGCTGAACCAGTCCAACTCCGCCTGGCCCTGCCTGCAGTACTGG  3961
 I  V  M  L  N  Q  L  N  Q  S  N  S  A  W  P  C  L  Q  Y  W

GATGAAGACTTAGTGGCTCGAGTCTTCCGGGTGCAGAACATCTCTCGGTTGCAGGAGGGA  4081
 D  E  D  L  V  A  R  V  F  R  V  Q  N  I  S  R  L  Q  E  G

TCCAAGAAGGCCTTCTTGCACCTGCTGGCTGAGGTGGACAAGTGGCAGGCCGAGAGTGGG  4201
 S  K  K  A  F  L  H  L  L  A  E  V  D  K  W D Q A  E  S  G

TGCGCCACGGTCCTGGAGATGATCCGCTGCCACAACTTGGTGGACGTTTTCTTTGCTGCC  4321
 C  A  T  V  L  E  M  I  R  C  H  N  L  V  D  V  F  F  A  A

TACGATGTGGCCCTGGAGTACTTGGAGGGGCTGGAGTCAAGATAGCGGGGCCCTGGCCTG  4441
 Y  D  V  A  L  E  Y  L  E  G  L  E  S  R
```

```
GCCTCCTGCTCTGCCCAAACACACTCCCATGGGGCAAGCACTGGAGTGGATGCTGGGCTA  4561
CCAAGGAGGAGCTTAGCAAGTCTGCACCCCACCCCCACCTCCATAGGGTCCTGCAGGCCT  4681
GGGACTCAGGCCAAGGGGGGTTGGCAGGATCCTGGGTTTTGGGAGGGATGAGTGAGGCCCT  4801
GATGTACTGGGACTTGGCATTTAGGATTCCATCTGGGGGACCCCCTGAAGGTCCCCCCCA  4921
AGCGCCCTCCTCCCCACTGCCCCCTCCAGCCCCTGAGATATTTTGCTCACTATCCCTCCC  5041
TCCCATGGGGGGGCTCCTTCCCTGCCTGACCCACTGTTGCAGAATGAAGTCACCTCGCCCC  5161
TCTGCAAGGCTGAACAACAGCCCCTGGGGTTGAGGCCCCTGTGGCTCCTGGTCAGGCTGC  5281
AGAGGTAGGACCAGTGCTTTTTTGTTTCTTTTGTTATTTTTGGTTGGGTGGGTGGGAAGG  5401
CTGTAGATATGACTACTGACCTACCTCGCAGGGGGCTGTGGGGAGGCATAAGCTGATGTT  5521
A                                                              5581
```

Fig. 2f